

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 7, line 9, with the following amended paragraph:

Figure 1 (A-D) shows a cDNA sequence (SEQ ID NO:1) of a hSMMMyHC variant using all exons (exons 1-43).

Please replace the paragraph beginning on page 7, line 13, with the following amended paragraph:

Figure 3 (A-D) shows a cDNA sequence (SEQ ID NO:3) of a hSMMMyHC variant missing exon 42 (uses exons 1-41 and 43).

Please replace the paragraph beginning on page 19, line 29, with the following amended paragraph:

The present invention provides an isolated hSMMMyHC polypeptide. Preferably, the polypeptide will comprise at least 50 contiguous amino acids of SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; ~~SEQ ID NO:10; SEQ ID NO:12~~, SEQ ID NO:10; SEQ ID NO:12; or SEQ ID NO:14. More preferably, the polypeptide comprises SEQ ID NO:2; SEQ ID NO:4; SEQ ID NO:6; SEQ ID NO:8; ~~SEQ ID NO:10; SEQ ID NO:12~~, SEQ ID NO:10; SEQ ID NO:12; or SEQ ID NO:14; or a substantially identical mutein, fragment, homolog, analog, or fusion protein thereof. According to a preferred embodiment, the polypeptide comprises the sequence -QGPSFAY- (i.e., ~~SEQ ID NO:16~~ SEQ ID NO:15; the insertion in the motor domain derived from the splice variant as described below). The polypeptides of this invention can also be fused in polypeptide linkage to a heterologous polypeptide sequence.

Please replace the paragraph beginning on page 24, line 28, with the following amended paragraph:

Bacteriophage antibody display libraries may also be screened for binding to a hSMMMyHC polypeptide, such as a full-length hSMMMyHC protein, a hSMMMyHC fragment, or a fusion protein comprising a hSMMMyHC polypeptide sequence comprising a hSMMMyHC epitope (generally at least 5 contiguous amino acids). Generally such hSMMMyHC peptides and the fusion protein portions consisting of hSMMMyHC sequences for screening antibody libraries comprise about at least 3 to 5 contiguous amino acids of hSMMMyHC, frequently at least 7 contiguous amino acids of hSMMMyHC, usually comprise at least 10 contiguous amino acids of hSMMMyHC, and most usually comprise a hSMMMyHC sequence of at least 14 contiguous amino acids.

Particularly preferred hSMMMyHC epitopes are:

-QGPSFAY- (~~SEQ ID NO:16~~ SEQ ID NO:15) and -CTEQGSHP- (~~SEQ ID NO:17~~ SEQ ID NO:16).

Please amend the paragraph beginning on page 30, line 4, with the following amended paragraph:

The human SMMMyHC gene has 43 exons of which are 2 exons (6 and 42) whose expression is variable and controllable by alternative splicing. Forms lacking exon 6, encoding 7 amino acids in the N-terminus, are largely found in the vasculature, forms containing exon 6 are visceral. Forms lacking exon 42 (SM1), are absent in fetal tissues; forms containing exon 42 (SM2) are more constitutively expressed. The sequence of all 4 possible splice variants are found in the Drawings;

Fig. 1 shows the hSMMMyHC isoform with all 43 exons represented (~~SEQ ID NO:1~~);

Fig. 3 shows the isoform which is missing exon 42 (~~SEQ ID NO:3~~).

Please amend the paragraph beginning on page 39, line 7, with the following amended paragraph:

Provided in the invention are polynucleotides comprising a segment encoding a hSMMyHC epitope or a multiplicity of hSMMyHC epitopes. A particularly preferred polynucleotide encoding a hSMMyHC epitope of the invention is comprises the sequence -CAAGGCCCATCTTTTGCCTAC- (~~SEQ ID NO:15~~) (SEQ ID NO:17).